

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 3, 2002, 23:06:20 ; Search time 56.46 Seconds
(without alignments)
2391.239 Million cell updates/sec

Title: US-09-497-822a-19
Perfect score: 4912
Sequence: 1 MEVQLGLGRVYPRPPSKTYR.....SVQVPLKLSGKVKPIYFHTQ 923

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues
Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL_17:*
- 1: sp-archaea:*
 - 2: sp-bacteria:*
 - 3: sp-fungi:*
 - 4: sp-human:*
 - 5: sp-invertebrate:*
 - 6: sp-mammal:*
 - 7: sp-mhc:*
 - 8: sp-organelle:*
 - 9: sp-phage:*
 - 10: sp-plant:*
 - 11: sp-rodent:*
 - 12: sp-virus:*
 - 13: sp-vertebrate:*
 - 14: sp-unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4777.5	97.3	906	Q9UN21	Q9un21 homo sapien
2	4341.5	88.4	896	Q9GKL7	Q9gkl7 sus scrofa
3	4298	87.5	895	Q9GKN9	Q9gkn9 sus scrofa
4	3822.5	77.8	730	Q13771	Q13771 homo sapien
5	2873	58.5	544	Q9BZG7	Q9bzg7 homo sapien
6	2857	58.2	542	Q9BZG6	Q9bzg6 homo sapien
7	2846.5	57.9	539	Q9NUA2	Q9nu22 homo sapien
8	2802.5	57.1	531	Q9BZG5	Q9bzg5 homo sapien
9	2414.5	49.2	780	P70048	P70048 xenopus lae
10	1676	34.1	344	Q91445	Q91445 serinus can
11	1639.5	33.4	853	Q93245	Q93245 oncorhynch
12	1604	32.7	303	Q97684	Q97684 ovis aries
13	1600	32.6	769	Q93497	Q93497 pagrus majo
14	1556	31.7	797	Q9PWG5	Q9pwg5 anguilla ja
15	1532	31.2	854	Q93244	Q93244 oncorhynch
16	1472.5	30.0	563	Q9YGV9	Q9ygv9 anguilla ja
17	1270	25.9	939	Q9DDJ4	Q9ddj4 halichoeres
18	1180.5	24.0	692	Q9GLWQ	Q9glwq canis fami
19				Q9W6F4	Q9w6f4 haplochromi

20	1179	24.0	732	13	Q9DDU9	Q9ddu9 xenopus lae
21	1157.5	23.6	583	13	Q9DEV4	Q9dev4 xenopus lae
22	1150	23.4	232	13	Q9IA30	Q9ia30 anolis caro
23	1125	22.9	710	13	Q9IBD5	Q9ibd5 anguilla ja
24	1064.5	21.7	360	13	Q42274	Q42274 crocodylus
25	1055	21.5	982	6	Q9N0W8	Q9n0w8 saimiri sci
26	978	19.9	232	6	Q9BE98	Q9be98 sus scrofa
27	966	19.7	348	13	Q91425	Q91425 cnemidophor
28	892	18.2	359	13	Q9IAC6	Q9iac6 oncorhynch
29	816	16.6	298	6	Q28547	Q28547 ovis aries
30	725.5	14.8	200	13	Q9I8F5	Q9i8f5 pinephales
31	715	14.6	166	13	Q91698	Q91698 xenopus lae
32	627	12.8	133	13	Q91426	Q91426 cnemidophor
33	590	12.0	258	6	Q9BDJ7	Q9bdj7 ovis aries
34	577	11.7	117	6	Q18925	Q18925 trichosurus
35	569	11.6	196	6	Q18991	Q18991 callithrix
36	568	11.6	110	6	Q97891	Q97891 macaca mula
37	479	9.8	169	11	Q63879	Q63879 rattus norv
38	461	9.4	569	13	Q98SM9	Q98sm9 brachydanio
39	458	9.3	91	6	Q18928	Q18928 macaca radi
40	451	9.2	95	6	Q97608	Q97608 didelphis m
41	444	9.0	95	6	Q97667	Q97667 macropus eu
42	443	9.0	526	6	Q9BDW5	Q9bdw5 sus scrofa
43	435	8.9	95	6	Q97622	Q97622 wallabia bi
44	417.5	8.5	484	5	Q9VSE9	Q9vse9 drosophila
45	410	8.3	125	6	Q18972	Q18972 bos taurus

ALIGNMENTS

RESULT 1

Q9UN21 ID Q9UN21 PRELIMINARY; PRT; 906 AA.

AC Q9UN21; 01-MAY-2000 (Tremblrel. 13, Created)

DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)

DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)

DI ANDROGEN RECEPTOR.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=MAMMARY CARCINOMA;

RA	Jin C.H., Urcan-Biseli M.S., Schrader W.T.;
RT	"Androgen Receptor" sequences in human mammary carcinoma MDA-MB-453 cells.;
RL	Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC	-1- SUBSEQUENCE LOCATION: NUCLEAR (BY SIMILARITY).
CC	-1- SIMILARITY: TO C4-TYPE STEROID RECEPTOR ZINC FINGER FAMILY.
DR	EMBL; AF162704; AD45921.1; -
DR	HSSP; P06536; IGDC.
DR	InterPro; IPR001103; Androgen_recep.
DR	InterPro; IPR000536; Hormone_rec_lig.
DR	InterPro; IPR001628; zf-C4.
DR	Pfam; PF02166; Androgen_recep; 1.
DR	Pfam; PF00104; hormone_rec; 1.
DR	Pfam; PF00105; zf-C4; 1.
DR	PRINTS; PRO0047; STROIDFINGER.
DR	SMART; SM00430; HOLI; 1.
DR	SMART; SM00399; ZNF_C4; 1.
DR	PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
KW	DNA-binding; Nuclear protein; Receptor; Transcription regulation; Zinc-finger.
SQ	SEQUENCE 906 AA; 97884 MW; 0A1FA8802B2EDDAF CRC64;

Query Match 97.3%
Best Local Similarity 97.8%
Matches 903; Conservative 1; Mismatches 2; Indels 17; Gaps 2;

Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
[1]
SEQUENCE FROM N.A.
TISSUE=PIUITARY;
Song J.H., Fahrtenkrug S.C., Rohrer G.A., Wise T.H., Ford J.J.;
"Sus scrofa androgen receptor (AR) coding sequence";
Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
[2]
SEQUENCE FROM N.A.
TISSUE=PIUITARY;
Song J.H., Fahrtenkrug S.C., Rohrer G.A., Wise T.H., Ford J.J.;
"porcine androgen receptor (AR) cDNA cloning: Expression in pituitary
associated with FSH secretion in boars";
Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILIARTY: TO C4-TYPE STEROID RECEPTOR ZINC FINGER FAMILY.
EMBL; AF202775; AAG37994.1; .
InterPro; IPR001103; Androgen_recep.
InterPro; IPR000536; Hormone_rec_lig.
InterPro; IPR001628; zf-C4.
Pfam; PF02166; Androgen_recep; 1.
Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; zf-C4; 1.
PRINTS; PR00047; STROIDFINGER.
SMART; SM00430; HOLI; 1.
SMART; SM00399; Znf_C4; 1.
PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
DNA-binding; Nuclear protein; Receptor; Transcription regulation;
zinc-finger.
SEQUENCE 896 AA: 97094 MW: 440F5F6E73BDC796 CRC64;

Query Match	88.4%;	Score 4341.5;	DB 6;	Length 899;
Best Local Similarity	88.4%;	pred. No. 6.9e-318;		
Matches 823; Conservative	17;	Mismatches 48;	Indels 43;	Gaps 4;

[illegible]

RESULT	2
Q29GKL7	
ID	Q9GKL7
AC	Q9GKL7
DT	01-MAY
DT	01-MAY
DT	01-JUN
DE	ANDRO

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Db 446 GSAGEAGAVPYGYTRPPQGLAGQEDLAIPIDIWPGVVSRYVPYSPSCVKSEMPWME 505
QY 533 SYSGPYGDMRLTETARDHVLPIIDYFPQKTCICGDEASGCHYGALTGCSCKVFFKRAAE 592
Db 506 SYSGPYGDMRLTETARDHVLPIIDYFPQKTCICGDEASGCHYGALTGCSCKVFFKRAAE 565
QY 593 GKQYLCASRNDCITDKFRKNCPSCLRKCYEAGMTLGARKLKLGNLKLOEAGEASST 652
Db 566 GKQYLCASRNDCITDKFRKNCPSCLRKCYEAGMTLGARKLKLGNLKLOEAGEASST 625
QY 653 TSPTTEETOKLTVSHTEGYEQPIFLNVLEAIEPGVVCAGHDNNQDPSFAALLSSINELG 712
Db 626 TSPTTEETOKLTVSHTEGYEQPIFLNVLEAIEPGVVCAGHDNNQDPSFAALLSSINELG 685
QY 713 EROLVHVVKWAKALPGFRNLHVDDQMAVIOYSWMGLMVFAMGWSRFTNVNSRMLYFAPDL 772
Db 686 EROLVHVVKWAKALPGFRNLHVDDQMAVIOYSWMGLMVFAMGWSRFTNVNSRMLYFAPDL 745
QY 773 VFEYRMHKSRYMSQCVRMHLSQDFGWLQITPQEFCLMKALLFSIIPVDGLKNQKFFD 832
Db 746 VFEYRMHKSRYMSQCVRMHLSQDFGWLQITPQEFCLMKALLFSIIPVDGLKNQKFFD 805
QY 833 ELRMNLIKELDRITIACKRNKPTSCSRFYQLTKLLDSVOPTARELHQFTFDLLIKSHMVS 892
Db 806 ELRMNLIKELDRITIACKRNKPTSCSRFYQLTKLLDSVOPTARELHQFTFDLLIKSHMVS 865
QY 893 VDFPEMMAEIIISVQPKILSGKVKPIYFHTQ 923
Db 866 VDFPEMMAEIIISVQPKILSGKVKPIYFHTQ 896

RESULT 3
O9GKN9 PRELIMINARY; PRT; 895 AA.
ID Q9GKN9
AC Q9GKN9;
DT 01-MAR-2001 (TremBLrel. 16, Created)
DT 01-MAR-2001 (TremBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TremBLrel. 17, Last annotation update)
DE ANDROGEN RECEPTOR AR.
OS Sus scrofa (Pig)
OC Eukaryota; Metazoa;
OC Mammalia; Euteleostomi;
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20539123; PubMed=11086548;
RA Trakooljul N., Ponsuksili S., Schellander K., Wimmers K.;
RT "A highly polymorphic repetitive polypyrimidine/polypurine (CCTTT)n
RT sequence in the 5' untranslated sequence of the porcine androgen
RT receptor gene.";
RL Anim. Genet. 31:288-289 (2000).
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: TO C4-TYPE STEROID RECEPTOR ZINC FINGER FAMILY.
DR EMBL; AF161717; AA040566.1; -.
DR InterPro; IPR001103; Androgen_recep.
DR InterPro; IPR000536; Hormone_rec_lig.
DR InterPro; IPR001628; zf-C4.
DR Pfam; PF02166; Androgen_recep; 1.
DR Pfam; PF00104; hormone_rec; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR00047; STROIDFINGER.
DR SMART; SM00430; HOLI; 1.
DR SMART; SM00399; znF_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
KW DNA-binding; Nuclear protein; Receptor; Transcription regulation;
KW Zinc-finger
SQ SEQUENCE 895 AA; 97156 MW; 923C2FDD1F7E4779 CRC64;
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Query Match 87.5%; Score 4298; DB 6; Length 895;
Best Local Similarity 87.7%; Pred. No. 1.1e-314;
Matches 816; Conservative 19; Mismatches 53; Indels 42; Gaps 4;
```

```
QY 1 MEVOLGLGRVYPRPKTYRGAFQNLFOVSREVIONPGRHPPEAASAPPGASLLLLLOOQ 60
Db 1 MEVOLGLGRVYPRPKTYRGAFQNLFOVSREVIONPGRHPPEAASAPPGASLLLLLOOQ 54
QY 61 QQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ 118
Db 55 -----QQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ 54
QY 119 SQPSALECHPERGCVPECAVAASKGLPQQLPAPPDEDDSAAPSTLSLGLPTFPGLSS 178
Db 101 SQQSAPCHPEPSGCTPEPGAASAASKGLQOQPPAPPDEDDSAAPSTLSLGLPTFPGLSS 160
QY 179 CSADLKDILSEASTMOLL-----QQQQQEAHSVSESSSGRAREASGAPTSSKDNVLYGGTST 233
Db 161 CSTDLKIDILSEAGTMOLLQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ 220
QY 234 ISDNARELCCKAVSVNGLGVEALEHLSPEQLRGDCMYAPLLGVPPAVRPTPCAPLAECK 293
Db 221 ISDAKELCKAVSVNGLGVEALEHLSPEQLRGDCMYAPLLTGPVSVRPTPCAPLAECK 280
QY 294 GSLDDDSAGKSTEDTAESYSPFKGYTKGLESLGSCGSAAGSSGTLELSTLSLYKSG 353
Db 281 GSLDDGPKSNEETAESYSPFKAGYTKGLDSESLGSCSGGEGSGGTLELSTLSLYKSG 340
QY 354 ALDEANAYOSRDYINFPPLALAGPPPPPPHPPHARIKLENPLDYCSAWAAAAACRYGDL 413
Db 341 ALDDVAAYPSRDYINFPPLALARPppppppppHPPHARIKLENPLDYCSAWAAAAACRYGDL 400
QY 414 ASLHGAGAGACGSGSPSAASSSWHTLTAEEOGLYGPCGGGGGGGGGGGGGGGGGG 473
Db 401 ASLHGAGAGCGSGSPSATSSSWHTLTAEESQLYGPC-----GGGGGG 445
QY 474 GGEAGAVAPYGYTRPPQGLAGQEDTAPDVWYPPGVMVSRVPYSPCTVKSEMPWMD 533
Db 446 SAGEAGAVAPYGYTRPPQGLAGQEDLAIPIDIWPGVVSRYVPYSPSCVKSEMPWME 505
QY 534 YSGPYGDMRLTETARDHVLPIIDYFPQKTCICGDEASGCHYGALTGCSCKVFFKRAAE 593
Db 506 YSGPYGDMRLTETARDHVLPIIDYFPQKTCICGDEASGCHYGALTGCSCKVFFKRAAE 565
QY 594 KQYLCASRNDCITDKFRKNCPSCLRKCYEAGMTLGARKLKLGNLKLOEAGEASST 653
Db 566 KQYLCASRNDCITDKFRKNCPSCLRKCYEAGMTLGARKLKLGNLKLOEAGEASST 625
QY 654 SPTEETOKLTVSHTEGYEQPIFLNVLEAIEPGVVCAGHDNNQDPSFAALLSSINELGE 713
Db 626 SPTEETOKLTVSHTEGYEQPIFLNVLEAIEPGVVCAGHDNNQDPSFAALLSSINELGE 685
QY 714 RQLVHVVKWAKALPGFRNLHVDDQMAVIOYSWMGLMVFAMGWSRFTNVNSRMLYFAPDL 773
Db 686 RQLVHVVKWAKALPGFRNLHVDDQMAVIOYSWMGLMVFAMGWSRFTNVNSRMLYFAPDL 745
QY 774 FNEYRMHKSRYMSQCVRMHLSQDFGWLQITPQEFCLMKALLFSIIPVDGLKNQKFFDE 833
Db 746 FNEYRMHKSRYMSQCVRMHLSQDFGWLQITPQEFCLMKALLFSIIPVDGLKNQKFFDE 805
QY 834 LRMYIKELDRITIACKRNKPTSCSRFYQLTKLLDSVOPTARELHQFTFDLLIKSHMVS 893
Db 806 LRMYIKELDRITIACKRNKPTSCSRFYQLTKLLDSVOPTARELHQFTFDLLIKSHMVS 865
QY 894 DFPEMMAEIIISVQPKILSGKVKPIYFHTQ 923
Db 866 DFPEMMAEIIISVQPKILSGKVKPIYFHTQ 895

RESULT 4
Q13771 PRELIMINARY; PRT; 730 AA.
ID Q13771
AC Q13771;
DT 01-NOV-1996 (TremBLrel. 01, Created)
DT 01-NOV-1996 (TremBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TremBLrel. 17, Last annotation update)
DE ANDROGEN RECEPTOR.
```

GN	AR.	Query Match	77.8%; Score 3822.5; DB 4; Length 730;
OS	Homo sapiens (Human).	Best Local Similarity	97.7%; Pred. No. 5e-279;
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Matches 721; Conservative	0; Mismatches 2; Indels 15; Gaps
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OC	NMBL_TaxID=9606;		
RN	[1]		
RC	SEQUENCE FROM N.A.		
RA	TISSUE=TESTIS;		
RA	MEDLINE=90258935; PubMed=2342476;		
RA	Govindan M.V.;		
RT	"Specific region in hormone binding domain is essential for hormone		
RT	binding and trans-activation of human androgen receptor.";		
RL	Mol. Endocrinol. 4:417-421(1990).		
CC	-!- SUBCELLULAR LOCATION: NUCLEUS (BY SIMILARITY).		
CC	-!- SIMILARITY: TO C4-TYPE STEROID RECEPTOR ZINC FINGER FAMILY.		
DR	EMBL; M73069; AAA51735.1; -		
DR	HSSP; P06536; LGDC.		
DR	InterPro; IPR001103; Androgen_recep.		
DR	InterPro; IPR000336; Hormone_rec_lig.		
DR	InterPro; IPR001628; zf-C4.		
DR	Pfam; PF02166; Androgen_recep; 1.		
DR	Pfam; PF00104; hormone_rec; 1.		
DR	Pfam; PF00105; zf-C4; 1.		
DR	PRINTS; PR00047; STROIDFINGER.		
DR	SMART; SM00430; HOLI; 1.		
DR	SMART; SM00399; znF_C4; 1.		
DR	PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.		
DR	DNA-binding; Nuclear protein; Receptor; Transcription regulation;		
KW	Zinc-finger.		
KW	SEQUENCE 730 AA; 79149 MW; 918B47C3B41B80C9 CRC64;		
QY	193 MQLLQQQQQBAVSEGGSSGRAREASGAPTSKDNVLGGTSTISDNAKELCKRAVSMGLG 252		
DB	1 MQLLQQQQQBAVSEGGSSGRAREASGAPTSKDNVLGGTSTISDNAKELCKRAVSMGLG 60		
QY	253 VEALHLSPEQLRGDCMYAPLLGVPPVAPRPTCAPLAECCKSLGDDSAKGSTEDTAEYS 312		
DB	61 VEALHLSPEQLRGDCMYAPLLGVPPVAPRPTCAPLAECCKSLGDDSAKGSTEDTAEYS 120		
QY	313 PFKGYTKGLEGESLGCSSAAAGSSGTLELPSTLSLYKSGALDAAAYQSRDYNFPLA 372		
DB	121 PFKGYTKGLEGESLGCSSAAAGSSGTLELPSTLSLYKSGALDAAAYQSRDYNFPLA 180		
QY	373 LAGPPPPPPHPHARIKLENPLDYGSAWAAAAOCRYGDLASLHGAGAGPGSGPSAA 432		
DB	181 LAGPPPPPPHPHARIKLENPLDYGSAWAAAAOCRYGDLASLHGAGAGPGSGPSAA 240		
QY	433 ASSSWHTLTFAEQLXPCGCGGGGGGGGGGGGGGGGGGGGGGAGAVAPYGYTRPPQG 492		
DB	241 ASSSWHTLTFAEQLXGPC-----GGGGGGGGGGGGGGGGGGGGGAGAVAPYGYTRPPQG 292		
QY	493 LAGQESDFTAPDVMVYPGMVSRYVPSPPTCKSEMGFWDSYSGPYGDMRLETARDHVL 552		
DB	293 LAGQESDFTAPDVMVYPGMVSRYVPSPPTCKSEMGFWDSYSGPYGDMRLETARDHVL 352		
QY	553 IDYFPPQKTCICGDEASGCHYCALTCGCKVFFKRAAEGKQKYLCA SRNDCITDKFRR 612		
DB	353 IDYFPPQKTCICGDEASGCHYCALTCGCKVFFKRAAEGKQKYLCA SRNDCITDKFRR 412		
QY	613 KNCPSCRLRKCYEAGMTLGARKLKKLGNLKLQEGEASSTTSPTETTKLVSHIEGYE 672		
DB	413 KNCPSCRLRKCYEAGMTLGARKLKKLGNLKLQEGEASSTTSPTETTKLVSHIEGYE 472		
QY	673 CQPIFLNVLEATPCVTCAGHDNNQPSFAALLSSLNELGERQLVHVWKWAKLPGRNL 732		
DB	473 CQPIFLNVLEATPCVTCAGHDNNQPSFAALLSSLNELGERQLVHVWKWAKLPGRNL 532		
QY	733 HVDQDMAVITQSWMGLMVFAMGWSRFTNVNSRMLYFAPDLVFNEMRHKSWYQCVRM 792		

Db	533	HYDDQMAVIQY	SWMGLVAFMGWRSFTNVASRMLYFAPDLVFNEMHKSRYMSQCVRM	592	
Qy	793	HLSQEFGWLQIT	POEFLCMKA-----LLLSFIIPVDGLKNOKFFDELRMNYIKELDR	845	
Db	593	HUSQEFGWLQIT	POEFLCMKAMLIFFFLLSFIIPVDGLKNOKFFDELRMNYIKELDR	652	
Qy	846	IACKRNKPTSCSR	RRFYQJTKLLDSVQPIARELHOFTELLIKSHMVSVDPEMMAELISV	905	
Db	653	IACKRNKPTSCSR	RRFYQJTKLLDSVQPIARELHOFTELLIKSHMVSVDPEMMAELISV	712	
Qy	906	QVPKILSGKVR	PIYFHTQ 923		
Db	713	QVPKILSGKVR	PIYFHTQ 730		
RESULT	5				
Q9BZG7					
ID	Q9BZG7	PRELIMINARY;	PRT:	544 AA.	
AC	Q9BZG7;				
DT	01-JUN-2001	(TrEMBLrel. 17, Created)			
DT	01-JUN-2001	(TrEMBLrel. 17, Last sequence update)			
DT	01-JUN-2001	(TrEMBLrel. 17, Last annotation update)			
DE	ANDROGEN RECEPTOR (FRAGMENT).				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
EN	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Magklara A., Diamandis E.P.;				
RT	"Poly-Q and poly-G repeats in				
RT	cancer cell line ZR-75-1";				
RL	Submitted (Nov-2000) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AF321911; AA039423.1				
KW	Receptor.				
FT	NON_TER				
SO	SEQUENCE	544 AA; 56013 MW;			
		544			
		544			
		CR64;			

[illegible]

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|||||
Db 421 AGAAGCGSGSPSAASSSWHTLFTAEAGLYGPGCGGGGGGGGGGGGGGGGGEA 480
QY 479 GAVAPYGYTRPPGGLAGQESDFTAPDVWYPGMWVSRVYPTCVKSEMPWMDSYSGPY 538
Db 481 GAVAPYGYTRPPGGLAGQESDFTAPDVWYPGMWVSRVYPTCVKSEMPWMDSYSGPY 540
QY 539 GDMR 542
Db 541 GDMR 544

RESULT 6
Q9BZG6 PRELIMINARY: PRT; 542 AA.
ID Q9BZG6
AC Q9BZG6;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE ANDROGEN RECEPTOR (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Magklara A., Diamandis E.P.;
RT "Poly-Q and poly-G repeats in the androgen receptor of the breast
RT cancer cell line T-47b.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF321915; AAK09425.1; -
DR InterPro; IPR001103; Androgen_recep.
DR Pfam; PF02166; Androgen_recep; 1.
KW Receptor.
FT NON_TER 542 542
SQ SEQUENCE 542 AA; 53628 MW; C363EF841CAF7739 CRC64;
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```
Query Match 58.2%; Score 2857; DB 4; Length 542;
Best Local Similarity 99.6%; Pred. No. 1.3e-206;
Matches 541; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 1 MEVOLGLGRVYPRPPSKTYRGAFQNLFSQSVREVIQNGPRHPEAASAPPASLILL-LQQ 59
Db 1 MEVOLGLGRVYPRPPSKTYRGAFQNLFSQSVREVIQNGPRHPEAASAPPASLILL-LQQ 60
QY 60 QQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ 119
Db 61 QQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ 120
QY 120 PQSALECHPERGCVPEPAAVAAASKGLPQLPAPPPDEDDSAAPSTLSLLGPTFFGLSSC 179
Db 121 PQSALECHPERGCVPEPAAVAAASKGLPQLPAPPPDEDDSAAPSTLSLLGPTFFGLSSC 180
QY 180 SADLKDILSEASTMQLLQOQQQAVSEGSSSGRAREASGAPTSSKDNLYLGTTISDNK 239
Db 181 SADLKDILSEASTMQLLQOQQQAVSEGSSSGRAREASGAPTSSKDNLYLGTTISDNK 240
QY 240 ELCKAVSVSMGLGVEALEHLSLPGCEQLRGDCMYAPLLGVPPAVRPTPCAPLAECKSLDD 299
Db 241 ELCKAVSVSMGLGVEALEHLSLPGCEQLRGDCMYAPLLGVPPAVRPTPCAPLAECKSLDD 300
QY 300 SAGKSTEDTAEYSPFKGGYTKGLESLGCGSAAAGSSGTLELPSTLSLYKSGALDEAA 359
Db 301 SAGKSTEDTAEYSPFKGGYTKGLESLGCGSAAAGSSGTLELPSTLSLYKSGALDEAA 360
QY 360 AYQSRDYNYFPLALAGPPPPPPHARIKLENPLDYGSAWAAAAAACRYGDLASLHGA 419
Db 361 AYQSRDYNYFPLALAGPPPPPPHARIKLENPLDYGSAWAAAAAACRYGDLASLHGA 420
QY 420 GAAGCGSGSPSAASSSWHTLFTAEAGLYGPGCGGGGGGGGGGGGGGGGGGGEAG 479
Db 421 GAAGCGSGSPSAASSSWHTLFTAEAGLYGPGCGGGGGGGGGGGGGGGGGGGEAG 479
QY 480 AVAPYGYTRPPGGLAGQESDFTAPDVWYPGMWVSRVYPTCVKSEMPWMDSYSGPY 539
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|||||
Db 480 AVAPYGYTRPPGGLAGQESDFTAPDVWYPGMWVSRVYPTCVKSEMPWMDSYSGPY 539
QY 540 DMR 542
Db 540 DMR 542

RESULT 7
Q9NUA2 PRELIMINARY: PRT; 539 AA.
ID Q9NUA2
AC Q9NUA2;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE DJ80804.1 (ANDROGEN RECEPTOR (DIHYDROTESTOSTERONE RECEPTOR))
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Chapman J.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Magklara A., Diamandis E.P.;
RT "Poly-Q and poly-G repeats in the androgen receptor of the breast
RT cancer cell line T-47b.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL049564; CAB87955.1; -
DR EMBL; AF321915; AAK09424.1; -
DR InterPro; IPR001103; Androgen_recep.
DR Pfam; PF02166; Androgen_recep; 1.
KW Receptor.
FT NON_TER 539 539
SQ SEQUENCE 539 AA; 55444 MW; AB493953B89D869F CRC64;
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Query Match 57.9%; Score 2846.5; DB 4; Length 539;
Best Local Similarity 99.4%; Pred. No. 8.2e-206;
Matches 539; Conservative 0; Mismatches 0; Indels 3; Gaps 2;

QY 1 MEVOLGLGRVYPRPPSKTYRGAFQNLFSQSVREVIQNGPRHPEAASAPPASLILL-LQQ 60
Db 1 MEVOLGLGRVYPRPPSKTYRGAFQNLFSQSVREVIQNGPRHPEAASAPPASLILL-LQQ 61
QY 61 QQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ 120
Db 59 QQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ 118
QY 121 PQSALECHPERGCVPEPAAVAAASKGLPQLPAPPPDEDDSAAPSTLSLLGPTFFGLSSC 180
Db 119 PQSALECHPERGCVPEPAAVAAASKGLPQLPAPPPDEDDSAAPSTLSLLGPTFFGLSSC 178
QY 181 ADLKDILSEASTMQLLQOQQQAVSEGSSSGRAREASGAPTSSKDNLYLGTTISDNK 240
Db 179 ADLKDILSEASTMQLLQOQQQAVSEGSSSGRAREASGAPTSSKDNLYLGTTISDNK 238
QY 241 LCKAVSVSMGLGVEALEHLSLPGCEQLRGDCMYAPLLGVPPAVRPTPCAPLAECKSLDD 300
Db 239 LCKAVSVSMGLGVEALEHLSLPGCEQLRGDCMYAPLLGVPPAVRPTPCAPLAECKSLDD 298
QY 301 SAGKSTEDTAEYSPFKGGYTKGLESLGCGSAAAGSSGTLELPSTLSLYKSGALDEAA 360
Db 299 SAGKSTEDTAEYSPFKGGYTKGLESLGCGSAAAGSSGTLELPSTLSLYKSGALDEAA 358
QY 361 YQSRDYNYFPLALAGPPPPPPHARIKLENPLDYGSAWAAAAAACRYGDLASLHGA 420
Db 359 YQSRDYNYFPLALAGPPPPPPHARIKLENPLDYGSAWAAAAAACRYGDLASLHGA 418
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QY 481 VAPYGYTRPPQGLAGQESDFTAPDVWYPGMVSRVYPSPCTCVKSEMPWMDSYSGPYGD 540
 Db 470 VAPYGYTRPPQGLAGQESDFTAPDVWYPGMVSRVYPSPCTCVKSEMPWMDSYSGPYGD 529
 QY 541 MR 542
 Db 530 MR 531
 RESULT 9
 P70048 PRELIMINARY; PRT: 790 AA.
 AC P70048;
 DT 01-FEB-1997 (Tremblrel. 02, Created)
 DT 01-JAN-1999 (Tremblrel. 09, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE ANDROGEN RECEPTOR ALPHA ISOFORM.
 GN XL ALPHA AR.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OC NCBI_TaxID=8355;
 [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE-93376782; PubMed=7690145;
 RA Fischer L., Catz D., Kelley D.;
 RT "An androgen receptor mRNA isoform associated with hormone-induced
 cell proliferation.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:8254-8258 (1993).
 [2]
 RN SEQUENCE FROM N.A.
 RP MEDLINE-95324753; PubMed=7601302;
 RA Fischer L.M., Catz D., Kelley D.B.;
 RT "Androgen-directed development of the Xenopus laevis larynx: control
 of androgen receptor expression and tissue differentiation.";
 RL Dev. Biol. 170:115-126 (1995).
 [3]
 RN SEQUENCE FROM N.A.
 RP Kamenetz F.R., Catz D.S., Fischer L.M., Kelley D.B.;
 RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
 [4]
 RN SEQUENCE FROM N.A.
 RP Kelley D.B., Kamenetz F.R., Kelley D.B., Badea T.C.;
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- SURCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -!- SIMILARITY: TO C4-TYPE STEROID RECEPTOR ZINC FINGER FAMILY.
 DR EMBL; U67129; AAC97386.1; -
 DR HSP; P65336; LGDC
 DR InterPro; IPR001103; Androgen_recep.
 DR InterPro; IPR000536; Hormone_rec_1lg.
 DR InterPro; IPR001628; zf-C4.
 DR Pfam; PF02166; Androgen_recep; 3.
 DR Pfam; PF00104; hormone_rec; 1.
 DR Pfam; PF00105; zf-C4; 1.
 DR PRINTS; PR00047; STROIDFINGER.
 DR SMART; SM00430; HOLI; 1.
 DR SMART; SM00399; ZnF_C4; 1.
 DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
 DR DNA-binding; Nuclear protein; Receptor; Transcription regulation;
 KW Zinc-finger.
 SQ SEQUENCE 790 AA; 86973 MW; 9E7FC136CCCC3906 CRC64;

Query Match 49.2%; Score 2414.5; DB 13; Length 790;
 Best Local Similarity 54.5%; Pred. No. 4.1e-173; Indels 209; Gaps 29;
 Matches 523; Conservative 65; Mismatches 162;
 QY 1 MEVQGLGVRYPSPKTYRGAFONLFSQVREVIONPGRHPEAASAPPASLLILQQQ 60
 Db 1 MEVHILGVRYPSPKTYRGAFONLFSQVREVIONPGRHPEAASAPPASLLILQQQ 51
 QY 61 QQQ 120

QY 421 AAGPGSGPSAAASSSWHTLFTAEQGLYPCGGGGGGGGGGGGGGGGGGGGGGGGG 480
 Db 419 AAGPGSGPSAAASSSWHTLFTAEQGLYPCGGGGGGGGGGGGGGGGGGGGGGGGG 477
 QY 481 VAPYGYTRPPQGLAGQESDFTAPDVWYPGMVSRVYPSPCTCVKSEMPWMDSYSGPYGD 540
 Db 478 VAPYGYTRPPQGLAGQESDFTAPDVWYPGMVSRVYPSPCTCVKSEMPWMDSYSGPYGD 537
 QY 541 MR 542
 Db 538 MR 539
 RESULT 8
 Q9BZG5 PRELIMINARY; PRT: 531 AA.
 AC Q9BZG5;
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE ANDROGEN RECEPTOR (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 [1]
 RN SEQUENCE FROM N.A.
 RP Magliara A., Dimandis E.P.;
 RT "Poly-Q and poly-G repeats in the androgen receptor of the breast
 cancer cell line MCF-7.";
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF321947; AAK04476.1; -
 KW Receptor.
 FT NON_TER 531 531
 SQ SEQUENCE 531 AA; 54419 MW; FA0D3AA60AC20DAB CRC64;

Query Match 57.1%; Score 2802.5; DB 4; Length 531;
 Best Local Similarity 98.0%; Pred. No. 1.6e-202;
 Matches 531; Conservative 0; Mismatches 0; Indels 11; Gaps 2;
 QY 1 MEVQGLGVRYPSPKTYRGAFONLFSQVREVIONPGRHPEAASAPPASLLILQQQ 60
 Db 1 MEVQGLGVRYPSPKTYRGAFONLFSQVREVIONPGRHPEAASAPPASLLILQQQ 57
 QY 61 QQQ 120
 Db 58 QQQ 110
 QY 121 PQSALCHPGRGCVPEPAAVAAKGLPOLPAPDEDDSAAPSTLSLLGPTFFGLSSCS 180
 Db 111 PQSALCHPGRGCVPEPAAVAAKGLPOLPAPDEDDSAAPSTLSLLGPTFFGLSSCS 170
 QY 181 ADLKDLSEASTMQLQQQQQAVSGSSSGRAREASGAPTSSKDNLYLGGTSTISDNAE 240
 Db 171 ADLKDLSEASTMQLQQQQQAVSGSSSGRAREASGAPTSSKDNLYLGGTSTISDNAE 230
 QY 241 LCKAVSMGLGVLEHLSPLGQRCDCMYAPLLGVPAVPTCAPLAECGSLDLS 300
 Db 231 LCKAVSMGLGVLEHLSPLGQRCDCMYAPLLGVPAVPTCAPLAECGSLDLS 290
 QY 301 AGKSTEDTAESPFGKGYTKGLESGILGSGSAAAGSSGTLEPSTLSLYKSGALDEAAA 360
 Db 291 AGKSTEDTAESPFGKGYTKGLESGILGSGSAAAGSSGTLEPSTLSLYKSGALDEAAA 350
 QY 361 YQSRDYNYFPLALAGPPPPPPHPIARIKLENPLDYGSAWAAAAAOCRYGDLASLHGAG 420
 Db 351 YQSRDYNYFPLALAGPPPPPPHPIARIKLENPLDYGSAWAAAAAOCRYGDLASLHGAG 410
 QY 421 AAGPGSGPSAAASSSWHTLFTAEQGLYPCGGGGGGGGGGGGGGGGGGGGGGGGG 480
 Db 411 AAGPGSGPSAAASSSWHTLFTAEQGLYPCGGGGGGGGGGGGGGGGGGGGGGGGG 469

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Db 52 -----:|||-----EASPDGT 68
QY 121 POSALECHPGCVPEGAANAASKGLPOOLPAPDDDDSAAPSTLSLLGPTFFGLSSCS 180
Db 69 PLNPWVTHP-----PAPWRE-AQAEAPON-PAGRTE-----GAQFPALGCP 109
QY 181 ADKDLSEASTMQLLQOQOQOEAUSGSSGRAREASGAPTSKDNKYLGGTSTISDNKE 240
Db 110 TELKEIL-----GEOSGRILESETP-AEKRGFGSGPEGISDSAKE 149
QY 241 LKAVSVMLGVEALEHLSPG---BQLRGDCMYAPLLGVPVAVRPTPCAPLAECCKGSL 297
Db 150 LKAVSVLSLSMEALEHLSAGAEQAQRGDCMYAH---PPDTH-KCQVAEEDKSDTR 203
QY 298 DD-----SAGKSTEDTAEYSPFKGGYTKLEGSCLSCGSAAGSGTLELST- 346
Db 204 DGPFRSSQSNFATGKSPED-----GGG-----GGGSSSAGGSEKEQCTD 246
QY 347 -----LSLYKSGA-LDEAAAYOSRDYNYNFFLALAGPPPPPPHP 385
Db 247 LALPEPAGYRHRAMELTPSLTYKPTAFMEESPGYPSRDFYSQMALA-----P 296
QY 386 HARIKLENPLDY-GSAWAAAAQCYGDLASLHGAGAGPCGSPSAASSSWHTLFTAE 444
Db 297 HGRIVKENPMYGGGAGAG---RYSEL-----SGFAHGCATAGWHTLF--E 339
QY 445 EQQLYPCGGGGGGGGGGGGGGGGGGGAGAVAPYGYTRPPGGLAGQESDFTAPD 504
Db 340 EGO-----SSGSFAEAG---PYSYPR-SHGPAAGAGEFPS-D 371
QY 505 VWPVG-GMVSRYVPSPCTVKSEMPWMDSYSGPYGDMRLTARDHVLPTDYFPQKTC 563
Db 372 AWYPAPTIGRVPISGP--MTEWAPMEGYPGAFGEMRLEGGRDHLPLTDYFPQKTC 429
QY 564 LIGDEASGCHYGALTCGCKVFFKRAEGKQKYLCAASRNDCTIDKFRKNCPSCLRKC 623
Db 430 LIGDEASGCHYGALTCGCKVFFKRAEGKQKYLCAASRNDCTIDKFRKNCPSCLRKC 489
QY 624 YEAGMTLGARKLKLGKLNKLOEAGEASTTSP-TEETTKLTVSHIEGYEQPIFLNVLE 682
Db 490 YEAGMTLGARKLKLGKLNKLOEAGEASTTSP-TEETTKLTVSHIEGYEQPIFLNVLE 549
QY 683 AIEPGVCAGHNNQPDFAALLSSNLGELQRLVHVVKWAKALPGFRLNHVDDQMAVYIQ 742
Db 550 AIEPVVWVWVWVWVWVWVWVWVWVWVWVWVWVWVWVWVWVWVWVWVWVWVWVWV 609
QY 743 YSWMGLVWVWVWVWVWVWVWVWVWVWVWVWVWVWVWVWVWVWVWVWVWVWVWVWV 802
Db 610 YSWMGLVWVWVWVWVWVWVWVWVWVWVWVWVWVWVWVWVWVWVWVWVWVWVWVWV 669
QY 803 ITPOEFLCMKALLFSIIPVDGLKNQKFDLRLMNYIKELDRITACKRKNPTSCSRFYQ 862
Db 670 ITPEFLCMKALLFSIIPVDGLKNQKFDLRLMNYIKELDRITACKRKNPTSCSRFYQ 729
QY 863 LTKLLDSVQPIARELHQFTFDLLIKSHMVSVDFPEMMAEIIISVQVPKILSGKRPYIFH 921
Db 730 LTKLLDSVQPIARELHQFTFDLLIKSHMVSVDFPEMMAEIIISVQVPKILSGKRPYIFH 788

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RESULT 10
Q91445 PRELIMINARY; PRT; 344 AA.
AC Q91445;
DT 01-NOV-1996 (TremBLrel. 01, Created)
DT 01-NOV-1996 (TremBLrel. 01, Last sequence update)
DE 01-JUN-2001 (TremBLrel. 17, Last annotation update)
DE ANDROGEN RECEPTOR (FRAGMENT).
GN AR.
OS Serinus canaria (Canary)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Fringillidae;
OC Carduelinae; Serinus.

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OX NCBI_TaxID=9135;
RN [1];
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RX MEDLINE=94130808; PubMed=8299561;
RA Nastluk K.L., Clayton D.F.;
RT "Seasonal and tissue-specific regulation of canary androgen receptor messenger ribonucleic acid."
RL Endocrinology 134:640-646 (1994).
CC 1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC 1- SIMILARITY: TO C4-TYPE STEROID RECEPTOR ZINC FINGER FAMILY.
DR EMBL; L25901; AAA17402.1;
DR HSP; P06536; IGLU.
DR InterPro; IPR000536; Hormone_rec_lig.
DR InterPro; IPR001723; Steroidhormone_receptor.
DR InterPro; IPR001628; zf-C4.
DR Pfam; PF00104; hormone_rec; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR00398; STRDHORMONER.
DR PRINTS; PR00047; STROIDFINGER.
DR SMART; SM00430; HOLI; 1.
DR SMART; SM00399; ZnF_C4; 1.
KW DNA-binding; Nuclear protein; Receptor; Transcription regulation;
KW Zinc-finger.
FT NON_TER 1 344
FT NON_TER 344 344
SQ SEQUENCE 344 AA; 39376 MW; 713676394FC0B030 CRC64;

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Query Match 34.1%; Score 1676; DB 13; Length 344;
Best Local Similarity 90.4%; Pred. No. 4.8e-118;
Matches 311; Conservative 20; Mismatches 13; Indels 0; Gaps 0;
QY 569 PASGCHYGALTCGCKVFFKRAEGKQKYLCAASRNDCTIDKFRKNCPSCLRKCYEAGM 628
Db 1 PASGCHYGALTCGCKVFFKRAEGKQKYLCAASRNDCTIDKFRKNCPSCLRKCYEAGM 60
QY 629 TLGARKLKLGKLNKLOEAGEASTTSP-TEETTKLTVSHIEGYEQPIFLNVLEAEPGV 688
Db 61 TLGARKLKLGKLNKLOEAGEASTTSP-TEETTKLTVSHIEGYEQPIFLNVLEAEPGV 120
QY 689 VCAGHNNQPDFAALLSSNLGELQRLVHVVKWAKALPGFRLNHVDDQMAVYIQSWMGL 748
Db 121 VCAGHNNQPDFAALLSSNLGELQRLVHVVKWAKALPGFRLNHVDDQMAVYIQSWMGL 180
QY 749 MVFAMGWRSTFNVNSRMLYFAPDLVFNEMRHSKRMYSQCVRMHLSQEFGLQITPOEF 808
Db 181 MVFAMGWRSTFNVNSRMLYFAPDLVFNEMRHSKRMYSQCVRMHLSQEFGLQITPOEF 240
QY 809 LCMKALLFSIIPVDGLKNQKFDLRLMNYIKELDRITACKRKNPTSCSRFYQTLKLLD 868
Db 241 LCMKALLFSIIPVDGLKNQKFDLRLMNYIKELDRITACKRKNPTSCSRFYQTLKLLD 300
QY 869 SVQPIARELHQFTFDLLIKSHMVSVDFPEMMAEIIISVQVPKILS 912
Db 301 SVTPIAKDLHQFTFDLLIKSHMVSVDFPEMMAEIIISVQVPKILS 344

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RESULT 11
Q93245 PRELIMINARY; PRT; 853 AA.
AC Q93245;
DT 01-NOV-1998 (TremBLrel. 08, Created)
DT 01-NOV-1998 (TremBLrel. 08, Last sequence update)
DE 01-JUN-2001 (TremBLrel. 17, Last annotation update)
DE ANDROGEN RECEPTOR (BETA).
GN AR-BETA.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]

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SEQUENCE FROM N.A.
Yamashita S.;
"Rainbow trout androgen receptor beta.";
Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY TO C4-TYPE STEROID RECEPTOR ZINC FINGER FAMILY.
EMBL; AB012096; BAA32785.1; -.
HSP; P06536; LGDC.
InterPro; IPR001103; Androgen_recep.
InterPro; IPR000536; Hormone_rec_lig.
InterPro; IPR001628; zf-C4.
pfam; PF02166; Androgen_recep; 1.
pfam; PF00104; hormone_rec; 1.
pfam; PF00105; zf-C4; 1.
PRINTS; PR00047; STROIDFINGER.
SMART; SM00430; HOLI; 1.
SMART; SM00399; ZnF_C4; 1.
PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
DNA-binding; Nuclear protein; Receptor; Transcription regulation;
Zinc-finger.
SEQUENCE 853 AA; 95776 MW; 65EFF5D3B36F4C4 CRC64;

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[illegible]

355 ETMEDKADYLQOQYSVKIKYEATSNBPAGTSQSYNGYNDNDNTQGP----- 404
Db
462 GGGGGGGGGGGGGEAGAVA-PGYTRPPQGLAGQESDFTAPDVWYPGCMVSRVPS 520
QY
405 ----RQMMNPSAGPDSGFCNPEYER-GGLYRER--PTSEQYPCGMLGRMPYNS 457
Db
521 TCVKRMGPWMDSYSGP7GDMRLFTARDHVLPIDYFFPQKCLICGDSASCHYGALTC 580
QY
458 PYLKNEVGWDLV----SVTDARFEGGRDHMPFEFFPQRTCLICADEASCHYGALTC 514
Db
581 GSKCVFFKRAEGKQYKLCASRNQCTDKFRKNCPSCLRUKCYEAGMTLGARKLKLGN 640
QY


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QY 684 IEPGVVCAAGHNNOPDFAALLSSNLGRLVHVYVVKAKALPGFRNLHVDDQMAVIOY 743
DB 121 IEPGVVCAAGHNNOPDFAALLSSNLGRLVHVYVVKAKALPGFRNLHVDDQMAVIOY 180
QY 744 SWMGLMVFAMGWSFTVNSRMILYFAPDLVFNEMHKSVMYVQVVRMRLHLSOEGWLOI 803
DB 181 SWMGLMVFAMGWSFTVNSRMILYFAPDLVFNEMHKSVMYVQVVRMRLHLSOEGWLOI 240
QY 804 TPQEFCLMKALLFSIIPVGLKNOKFDELNMNYIKELDRIIACKRKNTSCSRFYQL 863
DB 241 TPQEFCLMKALLFSIIPVGLKNOKFDELNMNYIKELDRIIACKRKNTSCSRFYQL 300
QY 864 TKL 866
DB 301 TKL 303

RESULT 13
O93497 PRELIMINARY; PRT; 769 AA.
AC O93497;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DE ANDROGEN RECEPTOR
OS Pagrus major (Red sea bream) (Chrysophrys major).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Sparidae; Chrysophrys.
OX NCBI_TaxID=811;
RN [1]
RP SEQUENCE FROM N.A.
RA Tounata K., Toyohata H.
RT "Red seabream androgen receptor."
RL Submitted (Aug-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY TO C4-TYPE STEROID RECEPTOR ZINC FINGER FAMILY.
DR EMBL; AB017158; BAA33451.1; -.
DR HSP; P06536; IRGD.
DR InterPro; IPR001103; Androgen_recep.
DR InterPro; IPR000536; Hormone_rec_lig.
DR InterPro; IPR001628; zf-C4.
DR Pfam; PF02166; Androgen_recep.
DR Pfam; PF00105; hormone_rec; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR00047; STROIDFINGER.
DR SMART; SM00430; HOLT; 1.
DR SMART; SM00399; ZnF_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
KW DNA-binding; Nuclear protein; Receptor; Transcription regulation;
KW Zinc-finger.
SQ SEQUENCE 769 AA; 86081 MW; 9305C627DBE42062 CRC64;

Query Match 32.7%; Score 1604; DB 13; Length 769;
Best Local Similarity 43.9%; Pred. No. 3.5e-112;
Matches 363; Conservative 79; Mismatches 171; Indels 214; Gaps 23;

QY 205 SEGSSSGRAFEASCA-PTSSKQNYL----- 228
DB 46 STGAGRMREADNADPNTYESGHMPLVCDMEKHCQCATAAQPQELFNADCRVDSRSF 105
QY 229 GGTSTISDNKELCKAVSVMGLGV-----ALEHLSPEGLRGDCWVAPLLGVPP 279
DB 106 SACATISETARELCKAVSVSLGLAMESNDPMDAALSOCAANDLGRLEYLFG----- 158
QY 280 AVPTPCAPLAECKGSLDSDAGKSTEDTAESYSPFGKGYTKGLESGLCSSAAAGSSG 339
DB 159 -----VGAAPLS-CPGA-----QAAYSEYKCPPEPLHGHK----- 188
QY 340 TLELPSTLSLYKSGALDEAAAYQSR-----DYNNPFLALAGPPPPPPHAPHRIKL 391

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DB 189 --QQOQLMDNFKS---SETGAHLQHLTSTPTVDEHNFTLCKAEDLTPRETAHQD----- 238
QY 392 ENPLDYGSAAAAAACRYGDLASLHGAGAAGPGS-----GSPSAAASSSWHTLFTAEGQ 447
DB 239 -----SVRAAACPY-----AQSLPGNMAHFGSP--APERFW-----Q 269
QY 448 LYGPCGGGGGGG-----GGGGGGGGG----- 469
DB 270 LYRPPDEAGDFGVMSRFRVTSYQPEQYSVKIKGEDTESAGALWGNVYTFNDRYNSQCV 329
QY 470 -----GGGGGGGAGAVAPYGYTRPPQGLAQESDFAPDVVYVPGMVSRVPPSPTCV 523
DB 330 GPRQCMNAHSTGANSALCHPY-----ERSVARPEHWYPGGML-RSPYPNSSYV 376
QY 524 KSEMGPNMDSYSGPYGDMRLETARDHVLPIDYFPQKTCICGDEASGCHYGALTCGSC 583
DB 377 KSEVGWLDV---PYSDPRFSDSSSEHMFMEFPFAQRMCLICDEASGCHYGALTCGSC 433
QY 584 KVFFKRAEGKQKYLCAASNDCTIDKFRKNCPCRLKCYEAGNTLGARKLKLGNLK- 642
DB 434 KVFEKRAAEGKQKYLCAASKNDCTIDKLRKNCPCRLKRCFEAGMTLGARKLKGQHN 493
QY 643 -----LQEEGASSTTSPTETTKLTVSHIEGYECQPIFLNVLEAIEPCVVCAGHDNN 696
DB 494 SDEHPLQEPAEVMPNISPKSGLS-----FNSQVFLNVLESIEPEVNVNAGHDY 543
QY 697 QPDSFAALLSSNLGRLVHVYVVKAKALPGFRNLHVDDQMAVIOYVSWMGLMVFAMGW 756
DB 544 QPDSAAATLLTSLNLEGERQLVVKVWAKGLPGFRNLHVDDQMTVIOHSMGMVAVFGLGW 603
QY 757 SFTNVNSRMILYFAPDLVFNEMHKSVMYVQVVRMRLHLSOEGWLOITPOEFLCMKALL 816
DB 604 SYKNVNGRMILYFAPDLVFNEMHKSVMYVQVVRMRLHLSOEGWLOITPOEFLCMKALL 663
QY 817 FSLIPVGLKNOKFDELNMNYIKELDRIIACKRKNTSCSRFYQLTKLLDSVQPIARE 876
DB 664 FSLIPVGLKNOKFDELNMNYIKELDRIIACKRKNTSCSRFYQLTKLLDSVQPIARE 876
QY 877 LHQFTFDLLIKSHMV--SVDPFPMMAEIIISVQPKILSGKVKPIYEH 921
DB 722 LHQFTFDLFGVQAQSLPTKVSFPEMIGELIISVHVPKILAGLAKPILFH 768

RESULT 14
O9PWG5 PRELIMINARY; PRT; 797 AA.
AC O9PWG5;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE ANDROGEN RECEPTOR-BETA
GN AR-BETA.
OS Anguilla japonica (Japanese eel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguilloidei;
OC Anguillidae; Anguilla.
OX NCBI_TaxID=7937;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RA MEDLINE=99395076; PubMed=10464240;
RA Ikeuchi T., Todo T., Kobayashi T., Nagahama Y.;
RT "cDNA cloning of a novel androgen receptor subtype."
RL J. Biol. Chem. 274:25205-25206 (1999).
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY TO C4-TYPE STEROID RECEPTOR ZINC FINGER FAMILY.
DR EMBL; AB025361; BAA83805.1; -.
DR HSP; P06536; IGDC.
DR InterPro; IPR001103; Androgen_recep.
DR InterPro; IPR000536; Hormone_rec_lig.
DR InterPro; IPR001723; Steroidhormone_receptor.
DR InterPro; IPR001628; zf-C4.

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QY 882 FDLLIKSHV--SVDFPEMMAEIIISVQVPKILSGKVPIYFH 921
 IIIIII: I:IIII:IIIIII:IIII: I:IIII: IIIII

DB 755 FDLFVQASLTKVNFPEMIAEIIISVHVPRILAGMAKPILFH 796

RESULT 15	
093244	PRELIMINARY; PRT: 854 AA.
AC	093244; Created
DT	01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT	01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE	ANDROGEN RECEPTOR ALPHA:

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AR-ALPHA.
ON Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
ON NCBI_TaxID=8022;
RX [1]
RN SEQUENCE FROM N.A.
RA Yamashita S.
RA "Rainbow trout androgen receptor alpha.";
RT Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RL -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: TO C4-TYPE STEROID RECEPTOR ZINC FINGER FAMILY.
CC EMBL; AB012095; BA32784.1; -.
DR HSSP; P06536; LGDC.
DR InterPro; IPR001103; Androgen_recep;
DR InterPro; IPR000536; Hormone_rec_lig.
DR InterPro; IPR001628; zf-C4.
DR Pfam; PF02166; Androgen_recep; 1.
DR Pfam; PF00104; hormone_rec; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR00047; STROIDFINGER.
DR SMART; SM00430; HOLI; 1.
DR SMART; SM00399; ZnF_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
KW DNA-binding; Nuclear protein; Receptor; Transcription regulation
KW zinc-finger.
OS SEQUENCE 854 AA; 96237 MW; 9F123B27874B0728 CRC64;

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Query Match	31.7%	Score 1556;	DB 13;	Length 854;
Best Local Similarity	39.8%	Pred. NO. 1.6e-108;		
			Indels 164;	Gaps 31;
			Microsches 298;	

[illegible]

DR PF02166; Androgen_recep: 1
 DR Pfam; PF00104; hormone_rec: 1.
 DR Pfam; PF00105; zf-c4: 1
 DR PRINTS; PRO0398; STRDOMERON.
 DR PRINTS; PRO0047; STROIDFINGER.
 DR PRINTS; PRO0047; STROIDFINGER.
 DR SMART; SM00430; HOLI: 1.
 DR SMART; SM00359; znf_C4: 1.
 DR PROSITE; PS00031; NUCLEAR_RECEPTOR.
 DR KWDNA-binding; Nuclear protein; Rec
 DR zinc-finger.
 DR SQ SEQUENCE 797 AA; 89924 MW; CFS

Query Match	32.6%	Score	1600	DB	13	Length	797
Best Local Similarity	43.0%	Pred.	No	7.4e-112			
Matches	379	Conservative	105	Mismatches	220	Indels	178
Gaps	27						
112	LDSEQQ-----PSQPS-ALECHPERGCVPEGAANAASKGLPQQLPAPPDDEDDSAAP	163					
21	LDTELQADSANPMPQPEAEARRIHFTKS-----SDSKGSDSIIL-----EPDNAQE	66					
164	STLSLLGPTPGPLSSCSADLKDILSEASTMQLLQOQQQAEVASEGSSSGRAEASGAPTSS	223					
67	NA-----YGPFLSLDHDCCTDOKSSLPTAPNRREINPHSDACYSNCSESA-----	113					
224	KDNYLGTGTSTISNAKELCKAVSVSGLGVAELEHLP-----GEOLRGDCMY-APL	274					
114	-----CTTISETARELCRAVSVGLGNDSNMENPEGNHNLASSUGSLDRKNFMEVPF	166					
275	LGVPVVRPTPCAPLAECCKSLDDSGAKSTEDTAIYSPFKGYTKGLGE-----	325					
167	LG---SSGTQESVPRAEVKCARLHD--GQLLONDELSGMKFTTHVQCLTNEVAPSHLSS	221					
326	-----SLGSGSAAAGSSCTLE-----LPSTLSLYKSGALDEAAA	360					
222	YSNMDTQETRLNABETETASKEQASCMDDAARSGFCQFOLLPTTLAQYSQ--IDPLSM	279					
361	-----YQSRDYNYFNFLALAGPPPPPPPHPHA-----RKLENPLDY-CSAWA	402					
280	GRSNFRSQFFYK-TLALANEAV-----EHAEGRYVDSSIQYSPKIKTENLQNOGSGW-	331					
403	AAAACQRYCDLASLHGAGAACPGSGSPSAAASSWHFLFTAESQQLYKPGCGGGGGGGG	462					
332	--DHQYRYNE-----NWHQYGPSRHGLHPYC-----	356					
463	GGGGGGGGGGGGGAGAVAYGYTRPPQGLAGQESDEFAPDWYVPGMYSRVPYSPTC	522					
357	-----TETNQFVVVEFDYQ-----GGGLLPDRSASESWFPGCMUKSPMTNLPC	403					
523	VKSEMGPMWDSYSGPYGD--MRLETARDHVLPIDYFFYPPOKTLCTCGDEASGCHYGALTCG	581					
404	LKTEVADMLVEV--PCSDRMLLGEGREHVPNMEFFFPQRTCLLCADEASGCHYGALTCG	460					
582	SKVFFKRAAEQKQYLCASRNDCITDKFRKNPCSRBLKCYEAGMTLGARKLKLGNL	641					
461	SKVFFKRAAEQKQYLCASRNDCITDKLRKNPCSRBLKCYEAGMTLGARKLKLQCL	520					
642	KLOEAGEASSTSPTEETTKLTVSHIEGYEQPTFLNVALEIPEGVVYACAGHDNNQPDSE	701					
521	KPDELPTQAPDAIQCISPKFGLS-----FPTQSVFLNILESIEPEVVYNAGHDQCOTDSA	576					
702	AALLSSLNELGERQLVHVHVKWAKALPGFRNLHVDDQMAVIQYSNMGLMVFAMGRSFTNV	761					
577	ATLLTSLNELGERQLFKVYKWKAGLPGFNHMHVDDQMTVIQHAMMGVWVFALGHRYSKYN	636					
762	NSRMLYFADPLVNEYRMHKSAMYSOCVRMRHLSQEFGLWLTPTQEFCLCMKALLFSIIP	821					
637	NARMLYFADPLVDNDRMRVRSSMYEHCIRMRHMSQEFVLLQVTHQEFCLCMKALLFSIIP	696					
822	VDGLKNQKFFDELRMVYIKELDRIIACKRNPTSCSRREYQLTKLKDSVOPIARELHOFT	881					
697	VEGLKNQKYPDDLNTYINFLDLINCNSRK--TNCRSQRIQLTRLMDSLQPIVKKLHOFT	754					

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Db 283 SSGHPC7DKOEFRLNENRDPTSKETDHELTGARSRSYHFDQLL-----PAHLAHF 334
QY 385 -----PHARIKLEPLDYGSAAWAAAQCRYGD-LASLHGAGAGPGSGSPSAAASS 436
Db 335 SOTETDRNSSHVYKPPAHVGE--TGETMEDYADYLOOQYSVKIKYEAFNRHNLPEPS 392
QY 437 W--HTLETAEBQOLYPCPGCGGGGGGGGGGGGGGAGAVAPYGYTRPPQCLA 494
Db 393 WFOYRYNDNDNTQVGL-----NSYIAGPDSALICNPHEYER--GGGLV 434
QY 495 GQESDFTAPDVWYPGGMVSRVPYPSPTCVKSEMGPMWDSYSGPYGDMRLETARDHVLPID 554
Db 435 RRER--PTEQWYPMGLRMPNPNPCIKNEVG---DSLDSVYTDARFEGGSDHMYPME 489
QY 555 YTFPOKTCLICGDEASGCHYGALTGCGCKVFFKRAAEGKOKYLCASRNDCITDKFRKN 614
Db 490 FFFPQRTCLICAEASGCHYGALTGCGCKVFFKRAAEGKOKYLCASRNDCITDKLRKN 549
QY 615 CPSCRLRKCYEAGMTLGARKLKLGNLKLQEEGEASSTTSPTETTKLTAVSHIEGYEQ 674
Db 550 CPSCRLRRCFAGMTLGTGRKLKIVQLKSPED--LPTQGT-DTIQGVSPQSLSFHSQ 606
QY 675 PIFNLVLEAIEPPGVVYVACAGHNNQDPSFAALLSSLNELGERQLVHVVKWAKALPGFRNLHV 734
Db 607 LVFLNILESIBPEVVHAGHDCQDPSAAALLTSLNELGERQLVHVVKWAKALPGFRNLHV 666
QY 735 DDOMAVIOYSWMLMVFAMGWRSTNVSRLYFAPDLVENEYRMHKSRYMOCVVRMHL 794
Db 667 DQMTVIOHSMWGMVYFGLGWRSYKNANCRLLYFAPDLVENDHRMHISSMFDHCIRROL 726
QY 795 SOEFCWLIQITPOEFLCMKALLFSIIPVDGLKNOKFFDELRMNYIKELDRIIACKRKNT 854
Db 727 SOEFLVLLQVTOEEFLCMKALLFSIIPVDGLKSOKYFDELRLTYINELGRVINYGRK--S 784
QY 855 SCSRRFYOLTKLDSVOPIARELHQFTFDLLIKSHMV--SVDFFPEMMAEIIISVQVKILS 912
Db 785 NCSORLYOLTRLMDSLQPVVVKLQQTFTDLFVQAQSLPTKVNFPEMIAEIIISVHLPKILA 844
QY 913 GKVKPIYFH 921
Db 845 GLAKPILFH 853

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Search completed: January 3, 2002, 23:12:25
Job time: 365 sec

